

Ec 941 REK----- 561
Tq 1060 ATPSVSAVFAGARAEKRE----- 1077
Pf 1254 MKRKKICTLNNKRANAKKVVHVNHLNEVVDKDTQLHKENNNNNMNSGNVENCKLKNKESYGYNNSSNCINTNNINIENNICHDISINKNIKVITNNSSNISNNENVTNLNCVSRAGSHHIYKKEKESIGSDDTNILSAQNSNNNFSCNNENMKNVDDVNVLE 1423
Bb 1071 PIDSK----- 1075
Tc 924 RM----- 925
Lm 922 RM----- 923
Sc 980 HG----- 981
Hs 933 PH----- 934

Ec 944 ----- 561
Tq 1078 ----- 1077
Pf 1424 NDTKKREDINTTTVMEGQNSVINNNKKNKENSLLKGEDEEDIVMVNLKKNENYSVINNVDCRKKMDMGKNINDECKTYKKNYKDMGLNINIIVDELNSGTSHSTNDHLYLDNFNTSDEEIGNKNMMDYLSKEKSISKNKPNGNSYVVVDVSVYNNYKINKMKELIDNENL 1593
Bb 1076 ----- 1075
Tc 926 ----- 925
Lm 924 ----- 923
Sc 982 ----- 981
Hs 935 ----- 934

Ec 944 ----- 561
Tq 1078 ----- 1077
Pf 1594 NDEYNNNNMNSNYNNASAFVNGKDRNDNLENDICEKNMDHTYKHYNRLNRRSTNERMMLMVNNEKESNHEKGHRNGLNKNKKNKMKGNKKNKKNYHYVNHKRNNENYNNIENSKFNNYVDDINKKEYYEDENDIYFFTHSSQGNDDLSNDNYSSEELNTD 1763
Bb 1076 ----- 1075
Tc 926 ----- 925
Lm 924 ----- 923
Sc 982 ----- 981
Hs 935 ----- 934

Ec 944 ----- 561
Tq 1078 ----- 1077
Pf 1764 EYDDDDYYDEDEDDYDDDDDDDDDDGEDEEDNDYNDGDYDYNLSSRSISDVSIIYSGNENIENKYNIDIGFKIIDNRNEKEKEKCKFIVLGCYRIGSSVEFDWSAIVHCKVTRKLNKHAAILNINCPETVSTDYDESRLYFDEITTEVIKFIYFNFSN 1933
Bb 1076 ----- 1157
Tc 926 ----- 1000
Lm 924 ----- 998
Sc 982 ----- 1056
Hs 935 ----- 1009

Ec 1019 GVIVYGGQTPKLARALEAAGVPIGTSFDAIDRAEDRERFQHAVERLKLKQANATVTAIEMAVEKAKEIGYPLVVRPSYVLGGRAMEIVYDEADLRRYFQTAVSVNDAPVLLDHFLLDDAVEVDVDAI--CDGEMVLIGGIMEHIEQAGVHSGDSACSLPAYTSLQE 805
Tq 1192 GVIIISVGGQTPNLTCSALEKQGVRIIGTSVAADCCEDRHKFSRLCDELNIDQPRWKEFTDLRTAKAPQEVGYVPLVVRPSYVLGGAAMRVVTDDEQLDAFLKIAAVVSGESPVVISKFVENAKEVEFDVSVACRGE--IVNFAISEHVENAGTHSGDATLILPGQKLYVET 1360
Pf 1934 GVIIAFGGQTSNNLVSFLYKNNVNLILGSHVHKLIVVVKIGINF--RTYVILKIDQPKWNKFTKLSKAIQFANEVKKFVPLVVRPSYVLGGAAMRVVNCPEELKNFLMKAIVSKDNPPVVISKFIENAKEIETIDCVSKNGK--IINYAISEHVENAGVHSGDATLILPAQNIYVET 2101
Bb 1158 GIVISVGGQTSNNLALQFHSGLPILGTSVESIDSCEDRYSFSEVVCVSGFDHDTCEMEFTSPEGAKQFCTKVSFPVLVVRPSYVLGGAAMRVVISPFELEKYLQTSAVVNRHEHPVVISKFIENAKEVEVEVTVVHLYGYTTETPLVEHVEHAGTHSGDATLILPAQNIYVET 1327
Tc 1001 GVVISLGGQIVQNMALRLKQGLPILGTPVNVKAENRHKFSKMCDELGVLPQEWLSTIEVQVHEFCQVGFPTLVVRPSYVLGGAAMRVVISAADINRYLEEAALVSGEHPVVVSKYEGAMEYDVIDVAHGR--VLCYAISEHVENAGVHSGDATMFLPPQNTKEV 1169
Lm 999 GVVISLGGQIVQNMALRLKQGLPILGTPANIDMAEDRNFKSKMCDNLGVPQEWISATSVEQVHEFCDRVGYPALVVRPSYVLGGAAMRVVIANKEDVTRYLKEASVSGEHPVVVSKYEDATEYDVIDVAHGR--VLCYGLISEHVENAGVHSGDATMFLPPQNTKDT 1167
Sc 1057 GVVISMGQTSNNIAMLHRENVKILGTSFDMIDSAENRYKFSRMLDQIGVDQPAWKEKLSMDEAESFAEKVGYVPLVVRPSYVLGGAAMRVVYSKNDLESYLNQAVEVSRDYPVVISKFIENAKEIEMDAVARNGE--LVMHVVSEHVENAGVHSGDATLIVPPQDLAPET 1225
Hs 1010 GVVISMGQTSNNIAMLHRENVKILGTSFDMIDSAENRYKFSRMLDQIGISQVRELSDLESARQCFQVGYPCVVRPSYVLGGAAMRVVAYADGDLERFLLSSAAVSKHEHPVVISKFIQEAKEIDVDAVASDGV--VAAIAISEHVENAGVHSGDATVTPPQDITAKT 1178

Ec 1188 QDVMRQQVQKLAFELQVRGLMNQVFAVK--NNEVYLIEVNPRARTVFPVSKATGVPLAKVAARVMAGKSLAEQGVTKVEIPYYSVKEVVLVFNKFPVGDPLPGLPEMRSTGEVMVGRTFAEAFAKAQLGSNSTMKKHGRALLSVREGDKER--VVDLAAKLLKQGFELD 972
Tq 1361 IRRVKKISQKLARALQVSGPFNIQFICK--QNDVKVIECNLRASRTFPFISKAFNVNLDLATAKVMIG--APVTPLPIHLMDLSFVVCVVPVFSFARLRCGDPVLGVEMRSTGEVACFGASKHEAFKALISAGVPLPLEKRTILISAGPLWSKMELEPYFKILLDGLGFTIY 1528
Pf 2102 HRKIKKISEKISKSLNISGPFNIQFICH--QNEIKIECNLRASRTFPFISKALNLFIDLATRILMG--YDVKPINSILIDLEYTAVKAPISFNRLHGSDCILGVEMRSTGEVACFGASKHEAFKALISAGVPLPLEKRTILISAGPLWSKMELEPYFKILLDGLGFTIY 2267
Bb 1328 HRAVKKIREFSRYLNYDGPFNQVLYCK--NNEIKIECNLRASRTLPFISKTLNLFIDQATRVVMVG--SPARVHNIQLMDIDYVAVKVPVFSFARLRCGDPVLGVEMRSTGEVACFGASKHEAFKALISAGVPLPLEKRTILISAGPLWSKMELEPYFKILLDGLGFTIY 1493
Tc 1170 MKRIYNTTALIAEELDVVGMNIIQFLFTKDKQLRVIEANIRSSRSVFPVSKTLGIFSPAVMVSFAFLSQHSDNLPVIKRARMTHIGCKASVFSFNRLAGADPLGVEMASTGEIVGFGRDKHEVFLKAMLCQNFRIY--QRGVFISCDVDAMAEDLCPPLS--ASDRFPV 1335
Lm 1168 MKRIYDVSNRVIAEELDVVGMNIIQFLFTKDKQLRVIEANIRSSRSVFPVSKTLGIFSPAVMVSFAFLSQHSDNLPVIKRARMTHIGCKASVFSFNRLAGADPLGVEMASTGEIVGFGRDKHEVFLKAMLCQNFRIY--QRGVFISCDVDAMAEDLCPPLS--ASDRFPV 1335
Sc 1226 VDRIVVATAKIGKALKITGPNYIQFIK--DNEIKVIECNLRASRSFPFISKVGVNLIELATAKIMG--LPLTPYVVEKLPDDYVAVKVPQFSFRLAGADPLGVEMASTGEIVGFGRDKHEVFLKAMLCQNFRIY--QRGVFISCDVDAMAEDLCPPLS--ASDRFPV 1391
Hs 1179 LERIKAVIHVAGQELQVTFPFLQLIK--DDQLKVEICNVRSRSPFVSKTLGVDLVALATRVIMG--EEVEPVGLMTG--SGVGVKVPQFSFRLAGADPLGVEMASTGEIVGFGRDKHEVFLKAMLCQNFRIY--QRGVFISCDVDAMAEDLCPPLS--ASDRFPV 1343

Ec 1355 AHTGTAIVLGEAGINPRLVNKHVEGRP-----HIQDRIKNGEYTIINTTSGR-----AIE [T. gondii Regulatory domain indel] -----DSRVIRRSALQYKHVYDTLNLGGFATAMALNADATEKVISVOEMHAQIK 1073
Tq 1529 ATEGTYDFYKFLSFPNVNKGSKFHQRLLK-----GLRTPPTAESDADACIRAKYASIRIRVRKPIVGSNESHNGGQSPHALSLESKGVEMVINVPDSMNRHAGTNGYLMRRTATDCGVPLLTNVKVASMFVEALNKEAKEAQGRSFDWTRSDWEYWPQKN 1688
Pf 2268 ATEGTYDFYKFLSFPNVNKGSKFHQRLLK-----VHNKNAENISPNITDLIMNKVEMVINITDTLKT-----KVSNGYKIRRLASDFQVPLITNMKLSLFDLSLYRKSFRQKERSYFTTKSYDYISLV 2391
Bb 1494 CYKGYIRIPLINEVPASGASITKGLDVSQ-----LLACSLQFEDTIGSLLHVGSSHKCGRLCCFNLRKVS-----PRPELMKSVVHFMAINAGCAIPNRLSDGVYMRRAAVDNKVTLITCMKLAFLIDALVMRHIRTSGKGLFFHNKSQOEYLN 1645
Tc 1336 TSKQTSRVLADYGIPTVTLQRHEDSE-----PTFDTAVAVKEKFDLVIQLRDKRDFMLRRCFQ-----ENATADYVIRRLAVDYNHSLTEPNVVMRFCEFTLDVVDVKEIEPEPFRLYVPRVYKMNENDNYTML 1460
Lm 1336 GTANTAVALHEHYGIECEVLLQRSSELPSGDACESNRPAVYDEEVAKKEKFDLVIQLRDKRDFMLRRCFQ-----ETAPPDYVIRRLAVDYNHSLTEPNVVMRFCEFTLDVVDVKEIEPEPFRLYVPRVYKMNENDNYTML 1469
Sc 1392 ATSGTADLSEHGIAVQLEVLNKKDDDDQKS-----EYSLTQHLANNEIDLINLPSANR--FRPPASV-----SKGYTRRLAVDYNHSLTEPNVVMRFCEFTLDVVDVKEIEPEPFRLYVPRVYKMNENDNYTML 1500
Hs 1344 ASLGTADPYTEHGKVTAVDWHFEEAVDGECP-----PQRSILEQLAEKNFELVINLSMRGAGGRRLSSFV-----TKGYTRRLAVDYNHSLTEPNVVMRFCEFTLDVVDVKEIEPEPFRLYVPRVYKMNENDNYTML 1455

Tc 1461 HRHKVGLCITSTNDKSVLAISLREEKIALTCFHACLGGIKNNSEEIAEQFRSISGTSRAHRHPH 1524
Lm 1470 RCHKVLMITDNNKSKVLAIRLSQEGELNI'CFPHGYLGG-----D-----IGQFEQAFQRP 1520